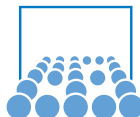


Towards Flexible Adaptive Molecular–Continuum Simulations

ICMMES 2012

Philipp Neumann and Wolfgang Eckhardt

25.07.2012



Contents

Motivation

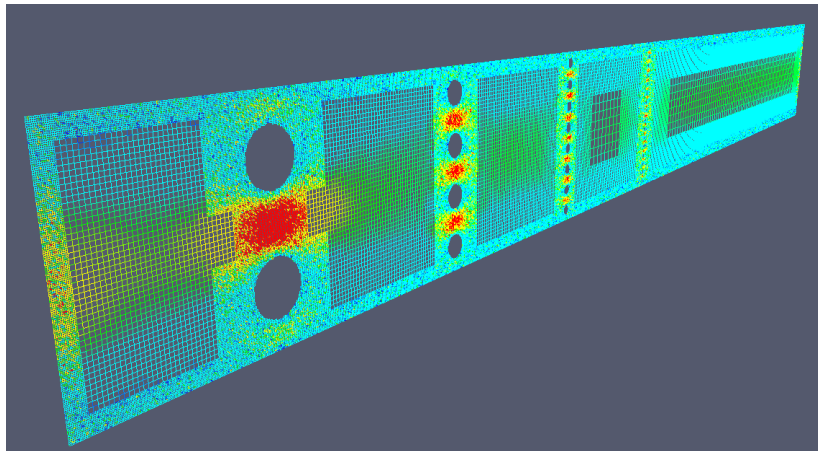
The Macro–Micro Coupling Tool (MaMiCo)

Validation

Coupled Scenarios

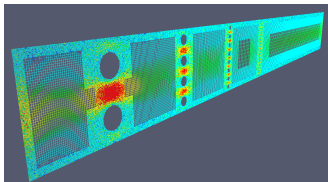
Conclusion & Outlook

Hybrid Molecular–Continuum Simulations: Why?



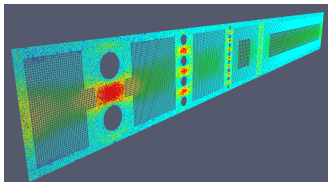
Hybrid Molecular–Continuum Simulations: Why?

- Huge interest in flows at micro- to nanoscale
→ Biosensors, micropumps, ...
- Nanoflows: May represent only small part of huge flow system
- Molecular Dynamics (MD) required to capture correct flow behaviour



Hybrid Molecular–Continuum Simulations: Why?

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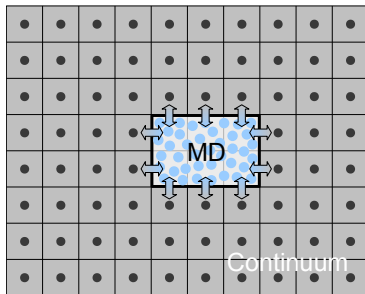


Computationally expensive
accurate MD simulations

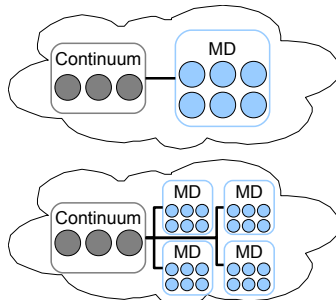


Less accurate computationally
cheap continuum simulations

Challenges: Physics & Distributed Computing



- Correct physical description at molecular–continuum interface
- Simple & fast testing of new coupling schemes



- Statistical noise on MD data¹
→ sampling
- Flexibility
- (Massively) Parallel implementation

N.G. Hadjiconstantinou, A.L. Garcia, M.Z. Bazant and G. He, Statistical error in particle simulations of hydrodynamic phenomena. J. Comput. Phys. 187, pp. 274–297, 2003.

Macro–Micro Coupling: Preparations

MD → Continuum:

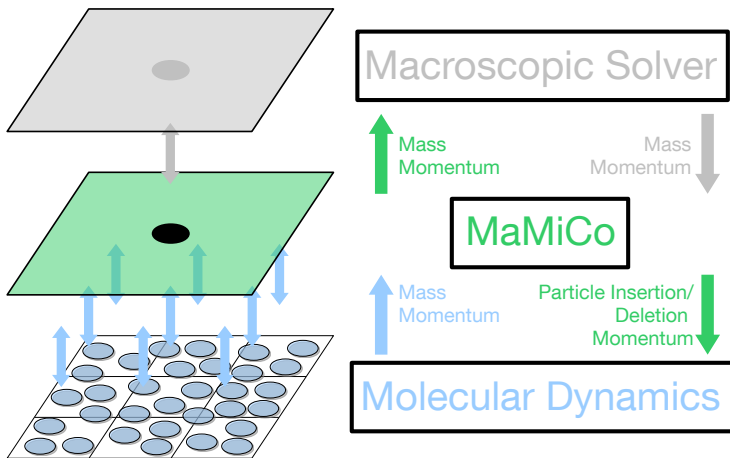
Mass exchange → average number of molecules
Momentum exchange → average velocities/ momentum
of molecules

Energy exchange

Continuum → MD:

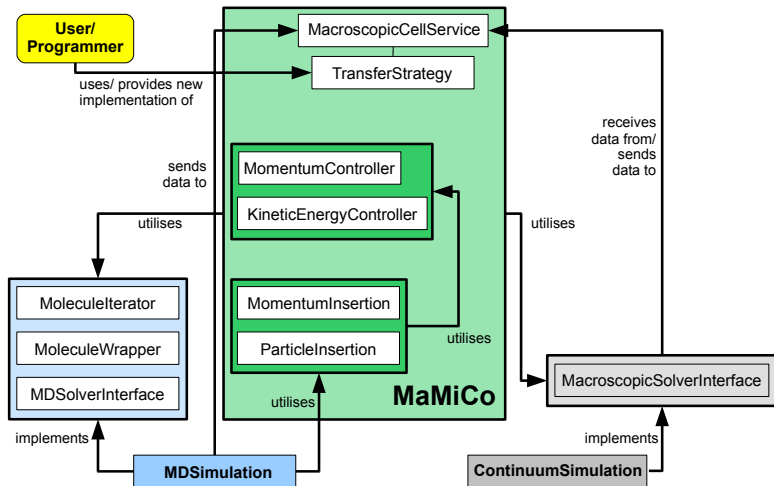
Mass exchange → insert/ delete molecules
Momentum exchange → in-/ decrease velocities of molecules
Energy exchange

The Macro–Micro Coupling Tool (MaMiCo) ¹

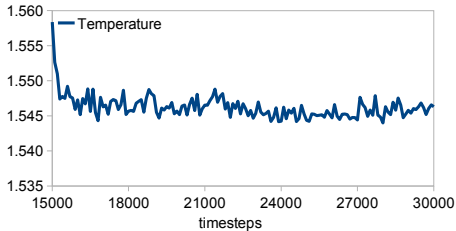
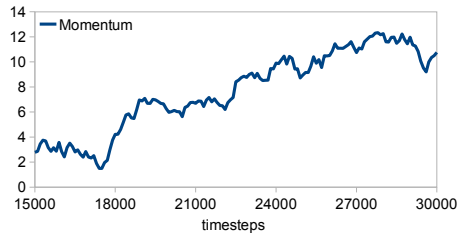
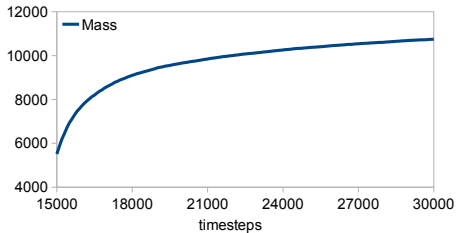


¹ P. Neumann and N. Tchipev, A Coupling Tool for Parallel Molecular Dynamics–Continuum Simulations. Proceedings of the 11th International Symposium on Distributed and Parallel Computing, München, 2012. Accepted.

The Macro–Micro Coupling Tool (MaMiCo)



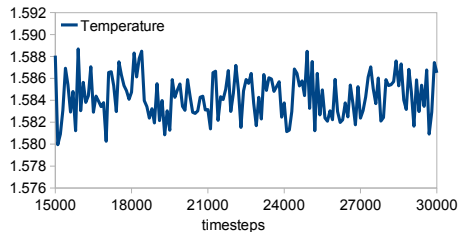
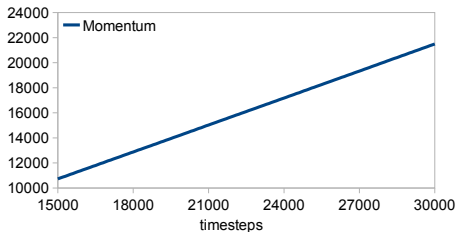
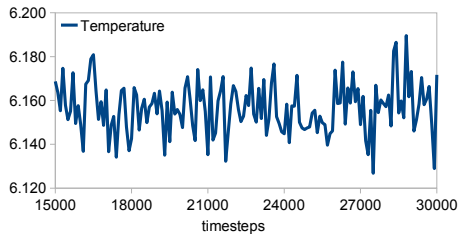
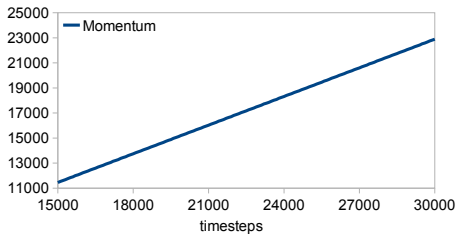
Validation: Mass Insertion



Experiment:

- Equilibrate MD system
- Double *number of molecules*
or
momentum
- Keep *momentum and temperature*
or
temperature constant

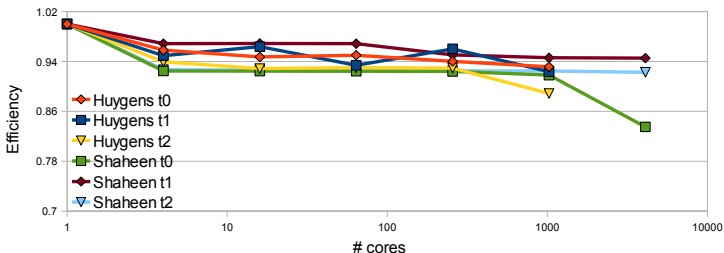
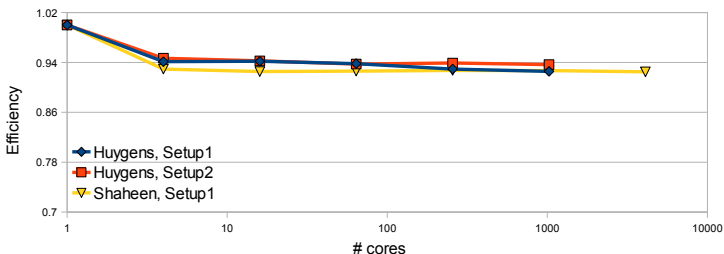
Validation: Momentum Insertion



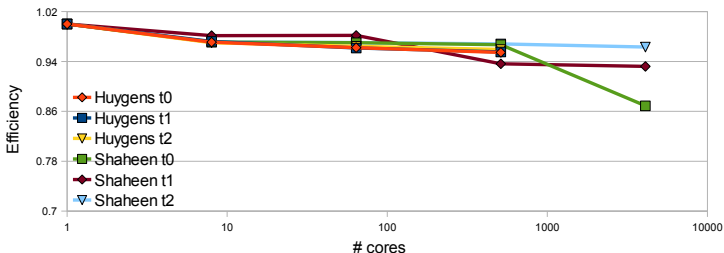
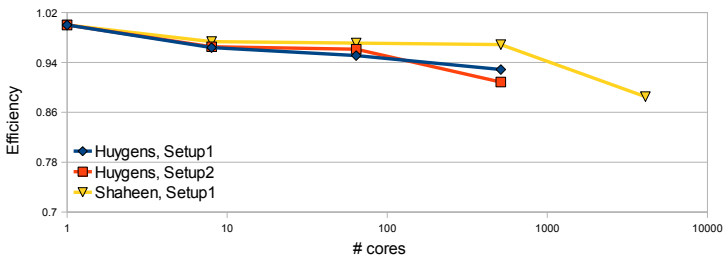
Runtimes

| Scenario | Runtime (s) | Timesteps/ Particle insertion | Timesteps/ Momentum insertion |
|----------------------------|-------------|-------------------------------------|-------------------------------------|
| MD($n = 0.40$) (2D) | 23.5 | 0 | 0 |
| MD($n = 0.78$) (2D) | 46.6 | 0 | 0 |
| Test A (2D) | 55.9 | 30 | 0 |
| MD($n = 0.80$) (2D) | 48.0 | 0 | 0 |
| Test B ($n = 0.80$) (2D) | 54.8 | 0 | 30 |
| MD($n = 0.40$) (3D) | 92.1 | 0 | 0 |
| MD($n = 0.78$) (3D) | 166.7 | 0 | 0 |
| Test A (3D) | 268.4 | 15 | 0 |
| MD($n = 0.80$) (3D) | 167.7 | 0 | 0 |
| Test B ($n = 0.80$) (3D) | 175.2 | 0 | 15 |

Parallel Particle Insertion: Results (2D)

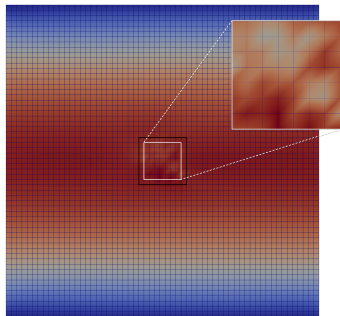


Parallel Particle Insertion: Results (3D)



LB–MD Coupling: Prototype

- Coupling between Mardyn¹ and Peano's Lattice Boltzmann component²
- Following the coupling approaches from Dupuis et al.³ and Werder et al.⁴
 - MD: 3D, LB: 2D
 - MD: Velocity relaxation in overlap regions
 - MD: RDF-based boundary forces
 - LB: Forcing terms for momentum exchange
- Fluctuations agree with theory



¹ M. Buchholz, Framework zur Parallelisierung von Molekulardynamiksimulationen in verfahrenstechnischen Anwendungen. PhD thesis. Institut für Informatik, Technische Universität München. Verlag Dr. Hut, München, 2010.

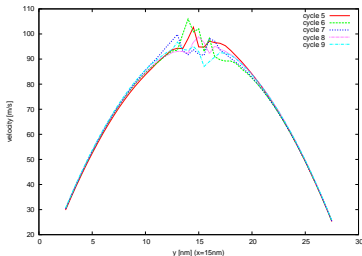
² P. Neumann and T. Neckel, A dynamic mesh refinement technique for Lattice Boltzmann simulations on octree-like grids. Comput. Mech., DOI 10.1007/s00466-012-0721-y, 2012. Published online.

³ A. Dupuis, E.M. Kotsalis and P. Koumoutsakos, Coupling lattice Boltzmann and molecular dynamics models for dense fluids. Phys. Rev. E 75 (046704), 2007.

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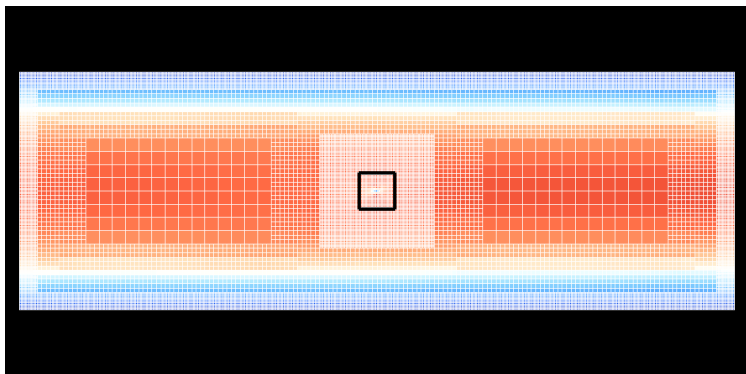
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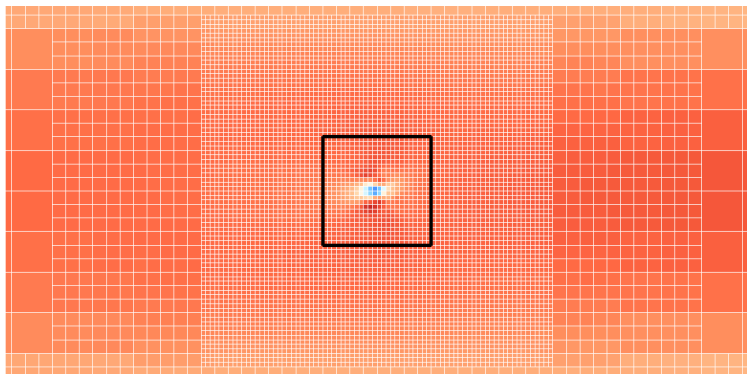
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LB-MD Coupling: Flow around CNT



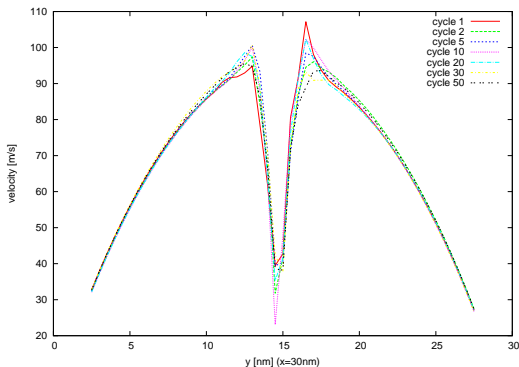
- Extension to adaptive grids
- Steady-state coupling:
22 000 MD iterations \Leftrightarrow
500 LB iterations
- MD: $n = 0.6$, $T = 1.8$
- 8000 single-centered LJ-atoms
- LB: Three grid levels, $Ma = 0.052$

LB-MD Coupling: Flow around CNT



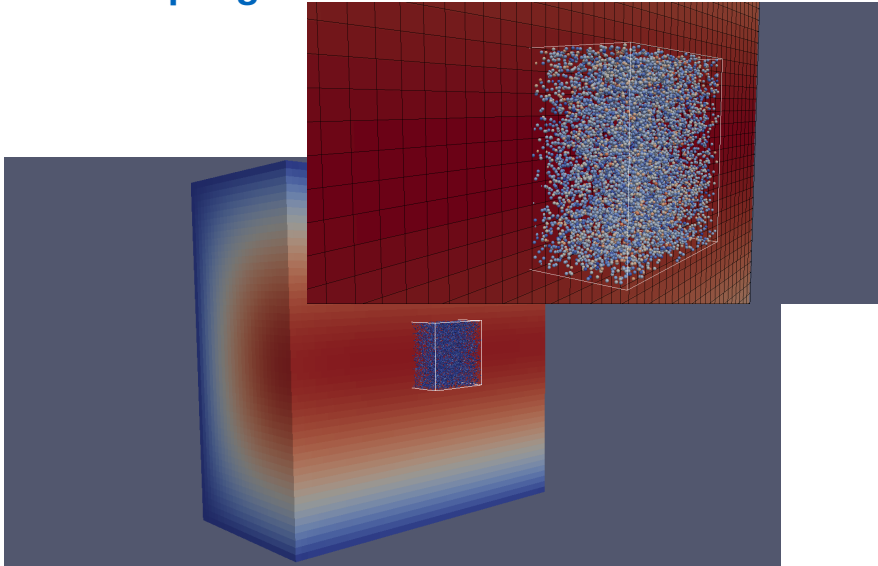
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LB-MD Coupling: MaMiCo



Conclusion & Outlook

Conclusion:

- Tool for hybrid molecular–continuum simulations (MaMiCo)
- 2D/ 3D support
- Distributed memory parallelisation

Outlook: From tests to parallel coupling algorithms

Thanks to:

Peter Hoffmann

Nikola Tchipev